

recommended

Page 1

Copyright (c) 1993 - 2000 Compugen Ltd.  
GenCore version 4.5

## OW nucleic - nucleic search, using sw model

Run on: January 24, 2002, 03:28:19 : Search time 222.28 Seconds  
(without alignments)  
347.126 Million cell updates/sec

Title: US-09-531-438-4

Perfect score: 90

Sequence: 1 atggabaaaaattttccaa.....gtccaatgaaaggaaatgtca 90

Scoring table: ORIGO\_NUC\_GePop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 98966

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

```
N_Genesed_1101:*
1: /SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq/NA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	
1	14	15.6	20 AA05048	PCR primer used to	
c	2	14	15.6	19 AAV07952	Helicobacter pylor
c	3	14	15.6	26 19 AAV07922	Helicobacter pylor
c	4	14	15.6	27 19 AAV07937	Helicobacter pylor
c	5	14	15.6	47 21 AAV68842	Human map related
c	6	13	14.4	17 16 ARQ92084	Renilla reniformis
c	7	13	14.4	20 ARX95307	PCR primer used to
c	8	13	14.4	23 22 ARU127610	Human lipoprotein
c	9	13	14.4	24 22 ARH55939	Human SCNA PCR-SS
c	10	13	14.4	26 15 ARQ68537	B. thuringiensis 33
c	11	13	14.4	26 21 ARQ67312	Alzheimer's disease

## SUMMARIES

C	12	13	13	14.4	26	21	AAC67342	Alzheimer's disease
C	13	13	13	14.4	31	19	AAV719577	Neisseria gonorrhoeae
C	14	13	13	14.4	34	16	AAT15377	ASF cosmid clone
C	15	13	13	14.4	35	22	AAFI207	Coxsackie B virus
C	16	13	13	14.4	36	22	AAFI207	Dissociation trans
C	17	13	13	14.4	38	17	AAT4130	13L promoter-HIV-
C	18	13	13	14.4	39	13	AAQ31530	HIV-2 env 3' fragm
C	19	13	13	14.4	39	14	AAQ31535	PCR primer HIVB2.
C	20	13	13	14.4	39	21	AAQ99138	Plasmid PromPTC PC
C	21	13	13	14.4	40	14	AAD0817	Insecticidal prote
C	22	13	13	14.4	40	21	AAZ01322	Primer 3A used to
C	23	13	13	14.4	40	21	AAZ01323	Primer 3B used to
C	24	13	13	14.4	41	19	AAV11009	Maize polymorphic
C	25	13	13	14.4	41	19	AAV51011	Male polymorphic
C	26	13	13	14.4	50	16	AAV215074	Human gene signature
C	27	13	13	14.4	50	20	AAVX21184	Synthetic plasmid
C	28	13	13	14.4	50	20	AAVS21048	Synthetic plasmid
C	29	12	13	13.3	17	18	AAV7046	Human fibrillar VEGF re
C	30	12	13	13.3	17	18	AAV70467	Human fibrillar VEGF re
C	31	12	13	13.3	17	20	AAAV1453	Integrin alpha 6 s
C	32	12	13	13.3	17	20	AAAV1454	Integrin alpha 6 s
C	33	12	13	13.3	17	20	AAAV1455	Integrin alpha 6 s
C	34	12	13	13.3	17	21	AAV31088	Hammerhead ribozym
C	35	12	13	13.3	17	21	AAV031090	Hammerhead ribozym
C	36	12	13	13.3	17	21	AAV031091	Hammerhead ribozym
C	37	12	13	13.3	17	21	AAAU081921	Hammerhead ribozym
C	38	12	13	13.3	18	21	AAAU081921	Human sigma 5' primer
C	39	12	13	13.3	19	15	AAO22806	Env gene 5' primer
C	40	12	13	13.3	19	21	AAZ19526	Human biallelic ma
C	41	12	13	13.3	19	21	AAZ19526	Human biallelic ma
C	42	12	13	13.3	20	11	AAQ05907	HIV mRNA translati
C	43	12	13	13.3	20	18	AAV72697	Staphylococcus aur
C	44	12	13	13.3	20	19	AAV72697	Corn kernel oil co
C	45	12	13	13.3	20	20	AAV92327	PCR primer used to
ALIGNMENTS								
RESULT	1							
ID.	AAZ05048	AAZ05048	standard:	DNA;	20	BP.		
AC	XX	XX						
XX	XX	XX						
DT	07-OCT-1999	(first entry)						
DE	PCR primer used to amplify an ORF of Chlamydia trachomatis.							
XX	Vaccine; eye disease; conventional trachoma; nonendemic trachoma;							
KW	paratrachoma; inclusion conjunctivitis; genital disease; perirectalitis;							
KW	nongonococcal urethritis; epidymitis; cervicitis; salpingitis; PCR primer;							
KW	bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.							
OS	Synthetic.							
OS	Chlamydia trachomatis.							
XX	W0928475-A2.							
PN	PD	10-JUN-1999.						
XX	PP	27-NOV-1998;	98W0-1B01939.					
XX	PR	04-NOV-1998;	98US-0107077.					
PR	28-NOV-1997;	97FR-0015041.						
PR	17-DEC-1997;	97FR-0016034.						
XX	PA	(GEST ) GENSET.						
PA	PI	Graffais R;						
XX	DR	WPI: 1999-371125/31.						



Copyright (c) 1993 - 2000 Compugen Ltd.

GenCore version 4.5

ON nucleic - nucleic search; using sw model

Run on: January 24, 2002, 02:22:33 : search time 93.51 Seconds  
(without alignments)  
(without alignments)  
791.983 million cell updates/sec

Title: US-09-531-438-3

Perfect score: 327

Sequence: 1 atttggatatacttaattttttcatgttttttatgtt 327

Scoring table: OUCG\_NDC

Gapop 60.0 , Gapext 60.0

Searched: 351203 seqs, 113238999 residues

Word size : ; 0

Total number of hits satisfying chosen parameters: 495388

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_ND:  
 1: /cgn2\_6/pctdata/2/ina/SA\_COMBO.seq: \*  
 2: /cgn2\_6/pctdata/2/ina/5B\_COMBO.seq: \*  
 3: /cgn2\_6/pctdata/2/ina/6A\_COMBO.seq: \*  
 4: /cgn2\_6/pctdata/2/ina/6B\_COMBO.seq: \*  
 5: /cgn2\_6/pctdata/2/ina/PCTUS\_COMBO.seq: \*  
 6: /cgn2\_6/pctdata/2/ina/Backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	4.9	29	3	US-09-816-977-12
2	16	4.9	36	1	US-09-629-60-16
3	15	4.6	27	1	US-09-120-827-66
4	15	4.6	27	1	PCT-US92-10793-3
5	15	4.6	30	5	PCT-US92-10793-3
6	15	4.6	32	1	US-09-856-61-29
7	15	4.6	32	3	US-09-852-299-29
8	14	4.3	18	2	US-09-205-20-20
9	14	4.3	29	3	US-09-816-977-12
10	14	4.3	30	2	US-09-629-01A-31
11	14	4.3	30	4	US-09-642-274D-110
12	14	4.3	36	1	US-09-629-600-16
13	14	4.3	37	2	US-09-403-853-8
14	13	4.0	18	3	US-09-847-44A-113
15	13	4.0	18	4	US-09-686-968-13
16	13	4.0	20	3	US-09-289-461-79
17	13	4.0	21	3	US-09-691-45-61
18	13	4.0	24	3	US-09-672-151
19	13	4.0	28	1	US-09-120-821-64
20	13	4.0	28	1	US-09-471-671-64
21	13	4.0	30	2	US-09-629-01A-79
22	13	4.0	30	4	US-09-612-74D-159
23	13	4.0	31	1	US-09-339-6380-5
24	13	4.0	31	2	US-09-706-746A-5
25	13	4.0	36	1	US-09-247-80A-14
26	13	4.0	36	2	US-09-711-728-14
27	13	4.0	37	2	US-09-097-554A-45

Sequence 10, Appl  
Sequence 10, Appl  
Sequence 45, Appl  
Sequence 45, Appl  
Sequence 10, Appl  
Sequence 45, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 40, Appl  
Sequence 168, App  
Sequence 168, App  
Sequence 55, App  
Sequence 168, App  
Sequence 19, Appl  
Sequence 39, Appl  
Sequence 11, Appl

RESULT 1  
US-09-816-977-12  
; Sequence 12, Application US/08816977  
; Patent No. 6080400  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
APPLICANT: Byrne, Lisa M.  
APPLICANT: Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
TITLE OF INVENTION: Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEES: Medien & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104

## ALIGMENTS

RESULT 1  
US-08-916-977-12

; Sequence 12, Application US/08816977

; Patent No. 6080400

GENERAL INFORMATION:  
APPLICANT: Williams, James A.

APPLICANT: Byrne, Lisa M.

APPLICANT: Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of

TITLE OF INVENTION: Verotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEES: Medien & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/816/977

FILING DATE: 13-Mar-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamlin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPHO-02450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 base pairs

TYPE: nucleic acid

STRANGENESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-16-977-12

Query Match 4.9%; Score 16; DB 3; Length 29;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 189 aaataataattttta 204

||||||||||||||||||

Db 9 AATAATTATTTTA 24

STATE: Virginia  
COUNTRY: U.S.A.

ZTC: 22202

RESULT 2

US-08-629-60-16

Sequence 16, Application US/08629600

PATENT NO. 5783196

GENERAL INFORMATION:

APPLICANT: NORIEGA, Fernando

APPLICANT: LEVINE, Myron M.

TITLE OF INVENTION: GUANOVANTS OF SHIGELLA AND VACCINES CONTAINING THE SAME

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGRIRE, MION, ZIHN, MACPEAK &amp; SEARS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/120,827

FILING DATE: 15-SER-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBIOL, NO. 5725496man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 714-158-0 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)413-3000

TELEFAX: (703)413-2220

TELEX: 24855 OPAT UR

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: RNA (genomic)

US-08-120-827-66

RESULT 3

US-08-629-60-16

Sequence 66, Application US/08629600

PATENT NO. 577346

GENERAL INFORMATION:

APPLICANT: KEENE, JACK D.

APPLICANT: KING, PETER H.

TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE

TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEAR ACIDS

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBIOL, SPIVAK, McCLELLAND, MAIER &amp; NEUSTADT,

ADDRESS: P.O.

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,675

FILING DATE: 07-JUN-1996

CLASSIFICATION: 556

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/120,827

FILING DATE: 15-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBIOL, NO. 577346man F.

Query Match Similarity 4.9%; Score 16; DB 1; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 aataatattttttta 204  
 Db 14 AATAATTATTTTA 29

Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



RESULT 4

Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26



Query Match Similarity 4.6%; Score 15; DB 1; Length 27;  
 Best Local Similarity 33.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 197 tattttttttttttaa 211  
 Db 12 UAUUUUUUUUAAA 26

<img alt="Diagram of mRNA structure showing a single strand with a

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.						
No.	Score	Query Match Length	DB	Length	DB ID	Description
1	16	4.9	29	6	AR09868	AR09868 Sequence
2	16	4.9	32	6	E27913	E27913 Method for
3	3	4.9	36	3	CEANONFR	X97532 C elegans D
4	4	4.9	36	6	AR019036	AR019036 Sequence
5	5	4.6	27	6	AR014030	AR014030 Sequence
11	15	4.6	27	6	I21980	I21980 Sequence 66
14	14	4.3	32	6	AR03189	AR03189 Sequence
15	14	4.3	29	6	AR07353	AR07353 Sequence
16	14	4.3	30	6	AR09868	AR09868 Sequence
17	14	4.3	30	6	AR028182	AR028182 Sequence
18	14	4.3	30	6	ARI38585	ARI38585 Sequence
19	14	4.3	32	6	E27913	E27913 Method for
20	14	4.3	36	6	AR019036	AR019036 Sequence
21	14	4.3	37	6	AR06204	AR06204 Sequence
22	13	4.0	45	6	AX049973	AX049973 Sequence
23	13	4.0	45	6	AX049974	AX049974 Sequence
24	13	4.0	20	6	AX098855	AX098855 Sequence
25	13	4.0	23	6	AX098856	AX098856 Sequence
26	13	4.0	24	6	A97479	A97479 Sequence 35
27	13	4.0	24	6	AX03544	AX03544 Sequence
28	13	4.0	24	12	AB059100	AB059100 Synthetic
29	13	4.0	25	6	AX02574	AX02574 Sequence
30	13	4.0	25	6	AX03268	AX03268 Sequence
31	13	4.0	26	6	AX036624	AX036624 Sequence
32	13	4.0	26	6	AX036624	AX036624 Sequence
33	13	4.0	28	6	AR04028	AR04028 Sequence
34	13	4.0	28	6	I21978	I21978 Sequence 64
35	13	4.0	29	6	AX012366	AX012366 Sequence
36	13	4.0	29	6	E59972	E59972 Highly acti
37	13	4.0	30	6	AR08230	AR08230 Sequence
38	13	4.0	30	6	AR18633	AR18633 Sequence
39	13	4.0	30	6	AX063379	AX063379 Sequence
40	13	4.0	31	6	I95122	I95122 Sequence 5
41	13	4.0	33	5	XELARSE59	K01606 xenopus lae
42	13	4.0	36	6	A41027	A41027 sequence 14
43	13	4.0	36	6	AR082586	AR082586 Sequence
44	13	4.0	36	6	AX16671	AX16671 Sequence
45	13	4.0	36	6	128261	128261 sequence 14
ALIGNMENTS						
RESULT	1					
AR099868		AR099868	29	bP	DNA	
LOCUS		DEFINITION	Sequence 12 from patent US 6080400.		PAT	14-FEB-2001
ACCESSION		VERSION	AR099868.1	GI:12810316		
KEYWORDS		SOURCE	Unknown.			
ORGANISM			Unknown.			
REFERENCE			Unclassified.			
AUTHORS			1 (bases 1 to 29)			
Williams, J.A. and Byrne, L.Marie.						

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

JOURNAL		Patent: US 5732467-A 30-JUN-1998;		and Immunoregulation	
FEATURES	Location/Qualifiers	Matched	15: Conservative	0: Mismatches	0: Indels
SOURCE		Qy	154 aaagggaaataaaa 168	Db	30 AACGGAAATATAAA 16
BASE COUNT	7 a 2 c 2 g	16 t			
ORIGIN					
RESULT	6				
AUTHORS	I21980				
TITLE	'I21980 27 bp DNA Sequence 66 from patent US 5525495.	PAT	07-OCT-1996		
DEFINITION					
LOCUS	I21980				
VERSION	I21980.1 GI:1602334				
ACCESSION					
FEATURES					
SOURCE	1. .27 /organism="unknown"				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 27)				
Keene,J.B., Levine,T. and Gac,F.					
Methods and compositions useful in the recognition, binding and expression of ribonucleic acids involved in cell growth, neoplasia and immunoregulation					
JOURNAL	Patent: US 5525495-A 66 11-JUN-1996;				
FEATURES					
SOURCE	1. .27 Location/Qualifiers				
BASE COUNT	7 a .2 c 2 g	16 t			
ORIGIN					
RESULT	7				
AUTHORS	I21980				
TITLE	'I21980 27 bp DNA Sequence 66 from patent US 5525495.	PAT	07-OCT-1996		
DEFINITION					
LOCUS	I21980				
VERSION	I21980.1 GI:1602334				
ACCESSION	I21980				
FEATURES					
SOURCE	1. .27 /organism="unknown"				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 29)				
Behnke,D., Schlotter,B., Albrecht,S., Guhrs,K. and Hartmann,M.					
Expression of signal-peptide-free staphylokinases					
JOURNAL	Patent: US 5801037-A 29 01-SEP-1998;				
FEATURES					
SOURCE	1. .32 Location/Qualifiers				
KEYWORDS					
SOURCE	/organism="unknown"				
BASE COUNT	3 a 8 c 4 g	17 t			
ORIGIN					
RESULT	8				
AUTHORS	AR07633/C				
TITLE	'AR07633 18 bp DNA Sequence 20 from patent US 5958772.	PAT	30-AUG-2000		
DEFINITION					
LOCUS	AR07633				
VERSION	AR07633.1 GI:10003099				
ACCESSION	AR07633				
FEATURES					
SOURCE	1. .18 Location/Qualifiers				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 18)				
Bennett,C. Frank, Ackermann,E.J. and Cowser,L.M.					
Antisense inhibition of cellular inhibitor of apoptosis-1 expression					
JOURNAL	Patent: US 5958772-A 20 28-SEP-1999;				
FEATURES					
SOURCE	1. .18 /organism="unknown"				
BASE COUNT	3 a 2 c 1 g	12 t			
ORIGIN					
RESULT	9				
AUTHORS	AR099868/C				
TITLE	'AR099868 29 bp DNA Sequence 12 from patent US 6080400.	PAT	14-FEB-2001		
DEFINITION					
LOCUS	AR099868				
VERSION	AR099868.1 GI:12810316				
ACCESSION	AR099868				
FEATURES					
SOURCE	1. .29 /organism="unknown"				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 29)				
Williams,J.A. and Byrne,L.Marie.					
Compositions for the prevention and treatment of verotoxin-induced disease					
JOURNAL	Patent: US 6080400-A 12 27-JUN-2000;				
FEATURES					
SOURCE	1. .29 Location/Qualifiers				
KEYWORDS					
SOURCE	/organism="unknown"				
BASE COUNT	11 a 2 c 5 g	11 t			
ORIGIN					
RESULT	10				
AUTHORS	AR028182				
TITLE	'AR028182 43% Score 14; DB 6; Length 29; Best Local Similarity 100.0%; Pred. No. 6.1e+04; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Origin Unknown.				
DEFINITION					
LOCUS	AR028182				
VERSION	AR028182.1 GI:12810316				
ACCESSION	AR028182				
FEATURES					
SOURCE	1. .32 /organism="unknown"				
KEYWORDS					
SOURCE	/organism="unknown"				
BASE COUNT	3 a 8 c 4 g	17 t			
ORIGIN					

Result No.	Score	Query Match	Length	DB	ID	Description
1	327	100.0	327	6	AX004614	AX004614 Sequence
2	327	100.0	1292	1	L77965	L77965 Clostridium
3	327	100.0	1392	6	AX004613	AX004613 Sequence
4	199	60.9	54310	1	AP003515	AP003515 Clostridi
5	81.8	25.0	12800	3	AE001429	AE001429 Plasmidu
6	7.9	24.2	3947	9	ALJ35906	ALJ35906 Human DNA
7	7.8	23.8	53332	2	AC023371	AC023371 Homo sapi
8	7.7	23.7	16343	2	AC006280	AC006280 Plasmidu
9	7.7	23.7	205129	2	AC005506	AC005506 Plasmidu
10	7.6.2	23.3	3302	3	AE003034	AE003034 Dicysteste
11	7.6.2	23.3	242513	2	AC079314	AC079314 Homo sapi
12	7.5.8	23.2	318221	2	PENALI3P3	AL049184 Plasmidu
13	7.5.8	23.1	14014	2	AE377947	AE377947 Oryza sat
14	7.5	22.9	17803	2	AC068119	AC068119 Homo sapi
15	7.4	22.8	15600	2	AC004153	AC004153 Plasmidu
16	7.3.2	22.4	863	11	CNS06EV0	AL395628 T7 end of
17	7.3	22.3	8622	8	YSCMCTOC	M97514 Saccharomye
18	72.8	22.3	34119	8	AE227178	AE227178 Chrysosid
19	72.2	22.1	10492	2	AC005504	AC005504 Plasmidu
20	72.2	22.1	16245	9	ALJ8151	ATJ58151 Human DNA
21	72.2	22.1	16566	2	AC004157	AC004157 Plasmidu
22	72.2	22.1	19982	9	ALJ354720	ALJ354720 Human DNA
23	72	22.0	15898	2	AC011146	AC011146 Homo sapi
24	71.6	21.9	18093	9	AC073409	AC073409 Homo sapi
25	71.6	21.8	12029	3	AE001400	AE001400 Plasmidu
26	71.4	21.8	17503	2	AC090014	AC090014 Homo sapi
27	71.2	21.8	11000	2	AL591074_2	Continuation (3 of
28	71	21.7	95477	9	AC007076	AC007076 Homo sapi
29	71	21.7	168799	9	AC009531	AC009531 Homo sapi
30	71	21.7	194338	9	AC010103	AC010103 Homo sapi
31	70.8	21.7	159475	2	AC021378	AC021378 Homo sapi
32	70.6	21.6	13433	3	AE315468	AE315468 Ceratitis
33	70.6	21.6	85779	3	SE01856	AT011856 Saccharom
34	70.6	21.6	12247	2	AC093220	AC093220 Homo sapi
35	70.6	21.6	159355	9	AE212831	AE212831 Homo sapi
36	70.6	21.6	161230	2	AC011355	AC011355 Homo sapi
37	70.6	21.6	234112	3	PRMLP2	AL035475 Plasmidu
38	70.6	21.6	340000	9	HS21C013	ALJ163213 Homo sapi
39	70.4	21.5	155456	2	AC027753	AC027753 Homo sapi
40	70.4	21.5	160524	9	AC060335	AC060335 Homo sapi
41	70.4	21.5	172158	2	AC022553	AC022553 Homo sapi
42	70.4	21.5	19951	2	AC006281	AC006281 Plasmidu
43	70.2	21.5	137342	9	ALJ392048	ALJ392048 Human DNA
44	70.2	21.5	180388	9	HUMREBLAS	L11910 Human retin
45	70.2	21.5	183584	9	AC012492	AC012492 Homo sapi
ALIGNMENTS						
RESULT 1	AX004614	LOCUS AX004614	327 bp	DNA	PAT	24-AUG-2000
DEFINITION Sequence 2 from Patent WO9915669.		ACCESSION AX004614				
VERSION AX004614.1	G1:9928055					
KWDS						
SOURCE	Clostridium perfringens.	ORGANISM				
	Clostridium perfringens	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;				
	Clostridium.					
	Bacteria; Firmicutes;					
REFERENCE 1 (bases 1 to 327)	Gibert,M. and Popoff,M.R.	compositions, Closridium toxin, and method for preparing immunogenic				
AUTHORS		Patent: WO 9915669-A 2 01-APR-1999; GIBERT MARIE (FRI); PASTEUR INSTITUT (FRI)				
JOURNAL		Location/Qualifiers				
FEATURES	source	1..327	/organism="Clostridium perfringens"			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

